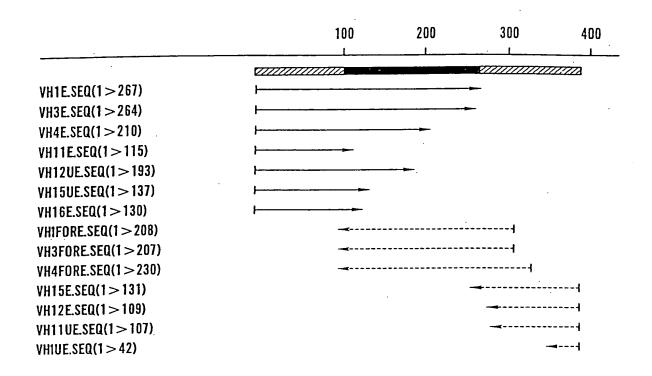


...

TREATMENT AND DIAGNOSIS OF CANCER INV: N. BANDER SN: 09/929,546

06/12



07/12

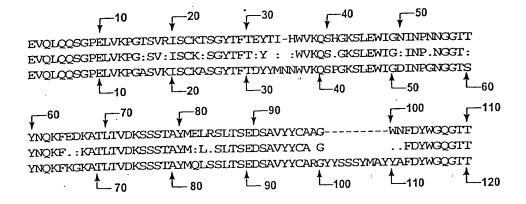
ENZYMES: ALL 74 ENZYMES (NO FILTER)
SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

Ddei Alul Avall Eco57 I	
Pst I	
SED. ID. NO. 1 TCTCCTGTCAGGAACTGCAGGTGTCCTCTCTGAGGTCCAACAGTCTGGACCTGGAACTGGTGAAG	
 	70 :
SEQ.ID.NO.2 ACAGGACAGICCTICACGICCACAGGACACTCCACGICGACTICGACCTICGACCACTICGACTICGACCACTICGACCACTICGACCACTICGACCACTICGACCACTICGACCACTICGACCACTICGACCACTICGACTICGACCACTICGACCACTICGACTICGACCACTICGAC	
SEQ.ID.NO.3 S P V R N C R C P L . G P A A T V W T . T G E SEO.ID.NO.4 L L S G T A G V L S E V Q L Q Q S G P E L V K	
SEQ.ID.NO.5 L S C Q E L Q V S S L R S S C N S L D L N W . S	
EcoR V	ı III Bsr I
Bsp6 II	
SEQ.ID.NO.1 CC1GGGACTTCAGTGAGGATATCCTGCAAGACTTCTGGATACACATTCACTGAATATACCATACACTGGG	10
SEQ. ID.NO. 2 GGACCCIGAAGICACICCIATAGGACGITCIGAAGACCITATGIGIAAGIGACITATATGGTATGIGACCC	
SEQ.ID.NO.3 A W D F S E D I L Q D F W I H I H . I Y H T L G SEO.ID.NO.4 P G T S V R I S C K T S G Y T F T E Y T I H W	
SEQ.ID.NO.5 L G L Q . G Y P A R L L D T H S L N T P Y T G	
Hph I Rsa I	
Nco I Kpn I	
SEQ.ID.NO.1 TGAAGCAGAGCCATGGAAAGAGCCCTTGAGTGGATTGGAAACATCAATCCTAACAATGGTGGTACCACCTA	^
	U
SEQ.ID.NO.3 EAEPWKEP. VDWKHQS.QWWYHL	
SEQ.ID.NO.4 V K Q S H G K S L E W I G N I N P N N G G T T Y	
SEQ.ID.NO.5 · S R A M E R A L S G L E T S I L T M V V P P	
Alúl Ban	11
10311	
· ¡Tag !Hae	
Tag 1 Acc 1 13a1	
SEQ.ID.NO.1 CAATCAGAAGTTCGAGGACAAGGCCACATTGACTGTAGACAAGTCCTCCAGTACAGCCTACATGGAGCTC	1
SEQ.ID.NO.1 CAATCAGAAGTTCGAGGACAAGGCCACATTGACTGTAGACAAGTCCTCCAGTACAGCCTACATCGAGCTC	1
SEQ. ID.NO.1 CAATCAGAAGTTCGAGGACAAGGCCACATTGACTGTAGACAAGTCCTCCAGTACAGCCCTACATGGACCTC SEQ. ID.NO.2 GTTAGTCTTCAAGCTCCTGTTCCGGTGTAACTGACATCTGTTCAGGAGGTCATGTCGGATGTACCTCGAG SEQ. ID.NO.3 Q S E V R G Q G H I D C R Q V L Q Y S L H G A	1
SEQ. ID. NO.1 CAATCAGAAGITGAGGACAAGGCCACATTGACIGIAGACAAGICCTCCAGIACAGCCTACATGCAGCIC SEQ. ID. NO.2 GITAGICITCAAGCTCCIGITCCGGIGIAACTGACATCTGITCAGGAGGICATGICGGATGIACCTCGAG SEQ. ID. NO.3 Q S E V R G Q G H I D C R Q V L Q Y S L H G A SEQ. ID. NO.4 N Q K F E D K A T L T V D K S S S T A Y M E L SEQ. ID. NO.5 T I R S S R T R P H . L . T S P P V O P T W S S	1
SEQ. ID.NO.1 CAATCAGAAGTTGAGGACAAGGCCACATTGACTGTAGACAAGTCCTCCAGTACAGCCTACATGCAGCTC SEQ. ID.NO.2 GTTAGTCTTCAAGCTCCTGTTCCAGTGTACCTCGAGTCAGGTCATGTCCAGTGTACCTCGAG SEQ. ID.NO.3 Q S E V R G Q G H I D C R Q V L Q Y S L H G A SEQ. ID.NO.4 N Q K F E D K A T L T V D K S S S T A Y M E L SEQ. ID.NO.5 T I R S S R T R P H . L . T S P P V Q P T W S S	30
SEQ. ID. NO.1 CAATCAGAAGITGAGGACAAGGCCACATTGACIGTAGACAAGTCCTCCAGTACAGCCTACATGCAGCTC SEQ. ID. NO.2 GTTAGICTTCAAGCTCCTGTTCCGGTGTAACTCACATCTGTTCAGGACGTCATGTCCGATGTACCTCGAG SEQ. ID. NO.3 Q S E V R G Q G H I D C R Q V L Q Y S L H G A SEQ. ID. NO.4 N Q K F E D K A T L T V D K S S S T A Y M E L SEQ. ID. NO.5 T I R S S R T R P H . L . T S P P V Q P T W S S SAU96	30
SEQ. ID. NO.1 CAATCAGAAGTTGAGGACAAGGCCACATTGACTGTAGACAAGTCCTCCAGTACAGCCTACATGCAGCTC SEQ. ID. NO.2 GTTAGTCTTCAAGCTCCTGTTCCAGTGTACACAACTCTGTTCAGCACGTCATGTCCAGTGTACCTCCAG SEQ. ID. NO.3 Q S E V R G Q G H I D C R Q V L Q Y S L H G A SEQ. ID. NO.4 N Q K F E D K A T L T V D K S S S T A Y M E L SEQ. ID. NO.5 T I R S S R T R P H . L . T S P P V Q P T W S S Alu I Sau96	1 30
SEQ. ID. NO.1 CAATCAGAAGITGAGGACAAGGCCACATTGACIGIACACCAGGCCTCCAGIACAGCCTCCAGIACAGCCTCCAGIACAGCCTCCAGIACAGCCTCCAGIACAGCCTCCAGIACAGCCTCCAGICAGCTCCAGICAGCTCCAGICAAGCTCCAGICAAGCTCCAGICAAGCTCCAGICAAGCTCCAGICAAGCTCCAGICAAGCTCCAAGCTCCAGICAAGCTCCAAGCTCCAGICAAGCTCCAAGCTCCAGICAAGCTCCAAGCTCCAGICAAGCTCCAAGCTCCAGICAAGCTCCAAGCTCCAGICAAGCTCCAAGCTCCAGICAAGCTCCAAGCTCCAGICAAGCTCCAGICAAGCTCCAGICAAGCTCCAGIACAGCTCCAGIACAGCCTCCAGIACAGCCTCCAGIACAGCCCTCAGICAAGCTCCAGIACAGCCCTCAGICAAGCTCCAGIACAGCCCTCAGICAAGCTCCAGIACAGCCCTCAGICAAGCTCCAGIACAGCCCTCAGICAAGCTCCAGIACAGCCCTACAITCAAGCTCCAGIACAGCCCTACAITCAAGCTCCAGIACAGCCCTACAITCAAGCTCCAGIACAGCCCTACAITCAAGCTCCAGIACAGCCCTACAITCAAGCTCCAGIACAGCACAITCAACACAGICCTCCAGIACAGCCCTACAITCAAGCTCCAGIACAGCCCTACAITCAAGCTCCAGIACAGCTCCAGIACAGCCCTACAITCAAGCTCCAGIACAGCTCCAGIACAGCCCTACAITCAAGCTCCAGIACAGCTCCAGICAAGCTCCAGICAAGCTCCAGICAAGCTCCAGICAAGCTCCAGICAAGCTCCAGICAAGTCCAGICAAGCTCCAGICAAGTCCACAGICAAGCCCCAAGTCCACAGICAAGCCCCAAGTCCACAGICAAGCCCCAAGTCCACAAGTCCACAGICAAGCCCCAAGTCCACAGICAAGCCCCAAGTCCACAGICAAGCCCCAAGTCCACAGCTCCAGICAAGCCCCAAGCTCCAAGCCCCAAGCTCCAAGCCCCAAGCTCCAAGCTCCAAGCTCCAAGCTCCAAGCCCCAAGCTCCAAGCCCCAAGCTCCAAGCCCCAAGCTCCAAGCCCCAAGCTCCAAGCTCCAAGCTCCAAGCCCCAAGCTCCAAGCCCCAAGCTCCAAGCCCCAAGCTCCAAGCCCAAGCCCCAAGCTCCAAGCCCCAAGCTCCAAGCCCCAAGCTCCAAGCCCAAGCTCCAAGCCCCAAGCTCCAAGCCCAAGCCCAAGCTCCAAGCCCAAGCTCCAAGCCCAAGCTCCAAGCCCAAGCCCAAGCTCCAAGCCCAAGCTCCAAGCCCAAGCTCCAAGCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCAAGCCCAAGCCAAGCCCAAGCCAAGCCCAAGCCAAGCCAAGCCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCAACAA	1 30
SEQ. ID. NO.1 CAATCAGAAGTTGAGGACAAGGCCACATTGACTGTACACAAGTCCTCCAGTACAGCCTACATGCAGCTC SEQ. ID. NO.2 GTTAGTCTTCAAGCTCCTGTTCCOGTGTAACCACATCTGTTCAGCACGTCATGTCCAGTGTACCTCCAG SEQ. ID. NO.3 Q S E V R G Q G H I D C R Q V L Q Y S L H G A SEQ. ID. NO.4 N Q K F E D K A T L T V D K S S S T A Y M E L SEQ. ID. NO.5 T I R S S R T R P H . L . T S P P V Q P T W S S Dde Hinf Pst	1 30 1 111
SEQ. ID. NO.1 CAATCAGAAGTTGAGGACAAGGCCACATTGACTGTAGACAAGTCCTCCAGTACAGCCTACATGCAGCTC SEQ. ID. NO.2 GTTAGTCTTCAAGCTCCTGTTCCGGTGTAACTGACACATCTGTTCAGGACGTCATGTCCGATGTACCTCGAG SEQ. ID. NO.3 Q S E V R G Q G H I D C R Q V L Q Y S L H G A SEQ. ID. NO.4 N Q K F E D K A T L T V D K S S S T A Y M E L SEQ. ID. NO.5 T I R S S R T R P H . L . T S P P V Q P T W S S Dde Hinf Pst Pvu	1 30 1 111
SEQ. ID. NO. 1 CAATCAGAAGTTGAGGACAAGGCCACATTGACTGTAGACAAGTCCTCCAGTACAGCCTACATGAAGCTC SEQ. ID. NO. 2 GTTAGTCTTCAAGCTCCTGTTCCGGTGTAACTGACATCTGTTCAGCAGGTCATGTCCGAGTGTACCTCGAG SEQ. ID. NO. 3 Q S E V R G Q G H I D C R Q V L Q Y S L H G A SEQ. ID. NO. 4 N Q K F E D K A T L T V D K S S S T A Y M E L SEQ. ID. NO. 5 T I R S S R T R P H . L . T S P P V Q P T W S S Dde Hinf Pst Pvu I	1 30 1 111
SEQ. ID. NO.1 CAATCAGAAGITGAGGACAAGGCCACATTGACTGTAGACAAGTCTCCAGTACAGCCTACATGACCTC SEQ. ID. NO.2 GITAGICTTCAAGCTCCIGITCCGGIGTAACTGACCATCTGTTCAGGACGTCATGTACCTCCAG SEQ. ID. NO.3 Q S E V R G Q G H I D C R Q V L Q Y S L H G A SEQ. ID. NO.4 N Q K F E D K A T L T V D K S S S T A Y M E L SEQ. ID. NO.5 T I R S S R T R P H . L . T S P P V Q P T W S S Dde Hinf! Pst	1 30 1 111
SEQ. ID. NO. 1 CAATCAGAAGTTGAGGACAAGGCCACATTGACTGTAGACAAGTCCTCCAGTACAGCCTACATGAAGCTC SEQ. ID. NO. 2 GTTAGTCTTCAAGCTCCTGTTCCGGTGTAACTGACATCTGTTCAGCAGGTCATGTCCGAGTGTACCTCGAG SEQ. ID. NO. 3 Q S E V R G Q G H I D C R Q V L Q Y S L H G A SEQ. ID. NO. 4 N Q K F E D K A T L T V D K S S S T A Y M E L SEQ. ID. NO. 5 T I R S S R T R P H . L . T S P P V Q P T W S S Dde Hinf Pst Pvu I	1 30 1 111
SEQ. ID.NO.1 CAATCACAACITCACACCACACACCACACTACACACCACTACACACCCTACATCACCCCCACTACACCCCTACATCACCCCCC	1 30 1 111
SEQ. ID. NO.1 CAATCAGAAGTTGAAGGACAAGTCACAATTGACTGTAGACAAGTCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAAGTTCAAGGACAAAGTCCAAGTCAAAGTCCAAGTCAACCTTGAAAACTCAATCAA	1 30 1 111
SEQ. ID. NO. 2 GITAGICITCAAGCICCIGITCCGGIGTAACICGACGAGGICATGICCAGTACAGCCTACATGCAGCTC SEQ. ID. NO. 2 GITAGICITCAAGCICCIGITCCGGIGTAACICACACTCIGITCAGAGGICATGICCGATGIACCTCGAG SEQ. ID. NO. 3 Q S E V R G Q G H I D C R Q V L Q Y S L H G A SEQ. ID. NO. 4 N Q K F E D K A T L T V D K S S S T A Y M E L SEQ. ID. NO. 5 T I R S S R T R P H . L . T S P P V Q P T W S S SEQ. ID. NO. 1 CCCACCCTAACATCTGAGGATTCTGCGAGGTCTATTATTGTGCAGCTGGTTGCAACTTTGACTACTGCGGGGGGGG	1 30 1 111
SEQ. ID. NO.1 CAATCAGAAGTTCAAGGACAAGGACAACGTGAACAAGTCCAGGTCAACGTCAAGTCCAAGATCCAAGACTCCAAAACTCCAAGACTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCCAAGTCCAAGTCCAAGACTCAAGACTAAACTCAAGTAAAGTAAGT	1 30 1 111
SEQ. ID. NO. 2 GITAGICITCAAGCICCIGITCCGGIGTAACICGACGAGGICATGICCAGTACAGCCTACATGCAGCTC SEQ. ID. NO. 2 GITAGICITCAAGCICCIGITCCGGIGTAACICACACTCIGITCAGAGGICATGICCGATGIACCTCGAG SEQ. ID. NO. 3 Q S E V R G Q G H I D C R Q V L Q Y S L H G A SEQ. ID. NO. 4 N Q K F E D K A T L T V D K S S S T A Y M E L SEQ. ID. NO. 5 T I R S S R T R P H . L . T S P P V Q P T W S S SEQ. ID. NO. 1 CCCACCCTAACATCTGAGGATTCTGCGAGGTCTATTATTGTGCAGCTGGTTGCAACTTTGACTACTGCGGGGGGGG	1 30 1 111

08/12

LIPMAN-PEARSON PROTEIN ALIGNMENT KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>115)	SEQ2(1>125)	SIMILARITY	GAP	GAP	CONSENSUS
J591VH.PRO	MUVHIIA.PRO	INDEX	NUMBER	LENGTH	LENGTH
(1>115)	(1>125)	75.6	2	10	125



LTVSS :TVSS VTVSS

09/12

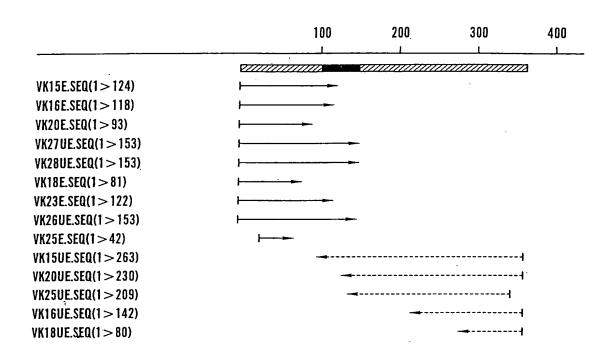


FIG. 9

10/12

ENZYMES:

SEQ.ID.NO.12 L H Q L Y

C

тΝ

SEQ.ID.NO.13

ALL 74 ENZYMES (NO FILTER):

SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

Hph I Alu TTATATGCAGCTGATGCGAACATTGTAATGACCCAATCTCCCAAATCCATGTCCATGTCAGTAGGAGAGA 70 SEQ.ID.NO.9 SEQ. ID.NO.10 AATATACCTOGACIACCCTTGTAACATTACTGGGTTAGAGGGTTTAGGTACAGGTACAGTCATCCTCTCT Y G A D G N I V M T Q S P K S M S M SEO. ID. NO. 11 PNLPNP C P C Q YMELMGTL SEQ. ID.NO.12 E, H C N SEQ.ID.NO.13 I Hae III Bsrl GGGTCACCTTGACCTGCAAGGCCAGTGAGAATGTGGTTACTTATGTTTCCTGGTATCAACAGAAACCAGA SEQ.ID.NO.9 SEQ. ID. NO. 10 CCCAGTGGAACTGGACGTTCCGGTCACTCTTACACCAATGAATACAAAGGACCATAGTTGTCTTTGGTCT SEQ.ID.NO.11 R V T L T C K A S E N V V T Y V S W Y Q Q K P E . PARPVRMWLLMFPGINRNQ G S P SEQ.ID.NO.12 LOGO ECGYL FLV ļΗ. SEO. ID. NO. 13 Mbo I Ava II |Dpn | Bsr I _lHpa II Bsa0 I Sau96 I Rsa i Alw261 Fok I Pvu I GCAGTCTCCTAAACTGCTGATATACGGGGCATCCAACCGGTACACTGGGGTCCCCGATCGCTTCACAGGC SEQ.ID.NO.9 SEQ. ID. NO. 10 OGTCAGAGGATTTGAGGACIATATGCCCCGTAGGTTGGCCCATGTGACCCCCAGGGGCTAGGTGTCCG Q S P K L L I Y G A S N R Y T G V P D R F T G SEQ.ID.NO.11 Y T G H P T G T L G S P IASQA SEQ.ID.NO.12 S S L L N C Ļ, SEQ.ID.NO.13 A.V. Mbo I Eco57 I Mbo II Bsp6 II _IDpn I AGTICATCTICCAACAGATTTCACTCTGACCATCAGCAGTGTGCAGGCTCAAGACCTTGCAGATTATCACT SEQ.ID.NO.9 SEQ. ID. NO. 10 TCACCTAGACGTTGTCTAAAGTGAGACTGGTAGTCGTCACACGTCCGAACGTCTGCAACGTCTAATAGTGA T L T I S S V Q A E D G S A T D F SEO. ID.NO.11 PSAVCRLKTL Q Ι VDLQQISL SEQ.ID.NO.12 SEQ.ID.NO.13 Q W I C N R F H S D H Q Q C A G C R L R P Ava li _IAlu 1 Sau96 I [Alu l ¡Rsa I SEQ.ID.NO.9 SEQ. ID.NO.10 CACCIGICCCAATGICGATAGGCATGIGCAAGCCICCCCCCTGGITCGACCTITATTITGCCCGACTACG IKRADA G G G TK L E SEQ.ID.NO.11 C G Q G Y S Y P Y Т F SEQ.ID.NO.12 V D R V T A I R T R S E G G P S W К NGLM R · G D Α G N T SEQ.ID.NO.13 TGCACCAACTGTA SEQ.ID.NO.9 SEQ.ID.NO.10 ACGIGGITGACAT APTV SEQ.ID.NO.11

11/12

LIPMAN-PEARSON PROTEIN ALIGNMENT KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>107)	SEQ2(1 > 1 1 1)	SIMILARITY	GAP	GAP	CONSENSUS
J591VK.PRO	MUVKV.PRO	INDEX	NUMBER	LENGTH	LENGTH
(1>107)	(1>109)	60.4	2	2	109

